

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sumitomo Chemical Company, Limited

(ii) TITLE OF INVENTION:

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sumitomo Chemical Company, Limited

(B) STREET: 5-33, Kitahama 4-Chome, Chuo-ku

(C) CITY: Osaka

(D) STATE: Osaka-fu

(E) COUNTRY: Japan

(F) ZIP: 541-0858

(G) TELEPHONE: 81-6-220-3405

(H) TELEFAX: 81-6-220-3390

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 1.4MB

(B) COMPUTER: IBM

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: Word 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:

(B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:

(B) TELEFAX:

(C) TELEX:

09026400-021998

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala Ala
1 5 10 15
Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser Asn
20 25 30
Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly Lys
35 40 45
Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala Ile
50 55 60
Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro Val
65 70 75 80
Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr
85 90 95
Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly Gln
100 105 110
Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala
115 120 125
Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala Asp

00492060 00196400 00000000

130 135 140
Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile
145 150 155 160
Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro
165 170 175
Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu Val
180 185 190
Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp
195 200 205
Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile Ile
210 215 220
Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ala
225 230 235 240
Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala Asp
245 250 255
Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met
260 265 270
Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu Ser
275 280 285
Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr
290 295 300
Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile Thr
305 310 315 320
Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu Ala

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325 330 335
Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg Ile
340 345 350
Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile Lys
355 360 365
Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe
370 375 380
Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp Asp
385 390 395 400
Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys
405 410 415
Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe Ala
420 425 430
Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser Phe
435 440 445
Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys
450 455 460 461

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 551 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala Asn Gly Leu Ala
1 5 10 15
Val Ala Ala Ala Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala
20 25 30
Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp Ala Asp Ala Asn
35 40 45
Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala Asn Gly Lys Ser
50 55 60
Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly Glu Ala Thr Ala
65 70 75 80
Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly His Ala Glu Ala
85 90 95
Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu Asp Ser Ala Ala
100 105 110
Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Ala Glu Glu Glu Glu
115 120 125
Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly Val Leu Ala Ala
130 135 140
Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr Lys Ile Ser Ala
145 150 155 160
Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro Leu Ala His Gly
165 170 175

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Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val Glu Ala Glu Asp
180 185 190

Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn Cys Tyr Pro Ala
195 200 205

Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala Glu His Leu Ser
210 215 220

Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val Phe Leu Thr Ala
225 230 235 240

Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val Leu Ala Gln Thr
245 250 255

Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr Pro Asn Tyr Glu
260 265 270

Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His Phe Asp Leu Ile
275 280 285

Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp Ser Leu Glu Ser Ile Ala
290 295 300

Asp Lys Asn Thr Thr Ala Met Val Ile Ile Asn Pro Asn Asn Pro Cys
305 310 315 320

Gly Ser Val Tyr Ser Tyr Asp His Leu Ser Lys Val Ala Glu Val Ala
325 330 335

Lys Arg Leu Gly Ile Leu Val Ile Ala Asp Glu Val Tyr Gly Lys Leu
340 345 350

Val Leu Gly Ser Ala Pro Phe Ile Pro Met Gly Val Phe Gly His Ile
355 360 365

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Thr Pro Val Leu Ser Ile Gly Ser Leu Ser Lys Ser Trp Ile Val Pro
370 375 380
Gly Trp Arg Leu Gly Trp Val Ala Val Tyr Asp Pro Arg Lys Ile Leu
385 390 395 400
Gln Glu Thr Lys Ile Ser Thr Ser Ile Thr Asn Tyr Leu Asn Val Ser
405 410 415
Thr Asp Pro Ala Thr Phe Ile Gln Ala Ala Leu Pro Gln Ile Leu Glu
420 425 430
Asn Thr Lys Glu Asp Phe Phe Lys Ala Ile Ile Gly Leu Leu Lys Glu
435 440 445
Ser Ser Glu Ile Cys Tyr Lys Gln Ile Lys Glu Asn Lys Tyr Ile Thr
450 455 460
Cys Pro His Lys Pro Glu Gly Ser Met Phe Val Met Val Lys Leu Asn
465 470 475 480
Leu His Leu Leu Glu Glu Ile Asp Asp Asp Ile Asp Phe Cys Cys Lys
485 490 495
Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro Gly Ser Val Leu Gly
500 505 510
Met Ala Asn Trp Val Arg Ile Thr Phe Ala Cys Val Pro Ser Ser Leu
515 520 525
Gln Asp Gly Leu Gly Arg Ile Lys Ser Phe Cys Gln Arg Asn Lys Lys
530 535 540
Arg Asn Ser Ser Asp Asp Cys
545 550 551

0 9 0 5 4 0 0 0 1 0 0 0

(A) ~~LENGTH:~~ 1660 base pairs

(A) ~~LENGTH~~: 1660 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY:

(ii) MOLECULAR TYPE: cDNA to mRNA

(iii) ~~HYPOTHETICAL:~~

(iv) ANTI-SENSE:

(V) FEATURE: CDS

(vi) LOCATION: 62 .. 1447

(vii) IDENTIFICATION METHOD: P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTGACTAGC TAGTTCATTC CCTGCCACAC TGCTAGTACT CCTCCTCGTT TCCTCGTGGC 60

A ATG GTA CAC CAG AGC AAC GGC CAC GGC GAG GCC GCC GCC GCC GCC 106

Met Val His Gln Ser Asn Gly His Gly Glu Ala Ala Ala Ala Ala

1 5 10 15

GCC AAC GGC AAG AGC AAC GGG CAC GCC GCC GCC GCG AAC GGC AAG AGC 154

Ala Asn Gly Lys Ser Asn Gly His Ala Ala Ala Ala Asn Gly Lys Ser

20 25 30

AAC GGG CAC GCG GCG GCG GCG GCG GTG GAG TGG AAT TTC GCC CGG GGC 202

Asn Gly His Ala Ala Ala Ala Ala Val Glu Trp Asn Phe Ala Arg Gly

35 40 45

AAG GAC GGC ATC CTG GCG ACG ACG GGG GCG AAG AAC AGC ATC CGG GCG 250

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Lys Asp Gly Ile Leu Ala Thr Thr Gly Ala Lys Asn Ser Ile Arg Ala
50 55 60
ATA CGG TAC AAG ATC AGC GCG AGC GTG GAG GAG AGC GGG CCG CGG CCC 298
Ile Arg Tyr Lys Ile Ser Ala Ser Val Glu Glu Ser Gly Pro Arg Pro
65 70 75
GTG CTG CCG CTG GCC CAC GGT GAC CCG TCC GTG TTC CCG GCC TTC CGC 346
Val Leu Pro Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg
80 85 90 95
ACG GCC GTC GAG GCC GAA GAC GCC GTC GCC GCC GCG CTG CGC ACC GGC 394
Thr Ala Val Glu Ala Glu Asp Ala Val Ala Ala Ala Leu Arg Thr Gly
100 105 110
CAG TTC AAC TGC TAC GCC GCC GGC GTG GGC CTC CCC GCC GCA CGA AGC 442
Gln Phe Asn Cys Tyr Ala Ala Gly Val Gly Leu Pro Ala Ala Arg Ser
115 120 125
GCC GTA GCA GAG CAC TTG TCA CAG GGC GTG CCC TAC AAG CTA TCG GCC 490
Ala Val Ala Glu His Leu Ser Gln Gly Val Pro Tyr Lys Leu Ser Ala
130 135 140
GAC GAC GTC TTC CTC ACC GCC GGC GGA ACT CAG GCG ATC GAA GTC ATA 538
Asp Asp Val Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile
145 150 155
ATC CCG GTG CTG GCC CAG ACT GCC GGC GCC AAC ATA CTG CTT CCC CGG 586
Ile Pro Val Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg
160 165 170 175
CCA GGC TAT CCA AAT TAC GAG GCG CGA GCG GCA TTC AAC AAG CTG GAG 634

00192050

Pro Gly Tyr Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Lys Leu Glu
180 185 190
GTC CGG CAC TTC GAC CTC ATC CCC GAC AAG GGG TGG GAG ATC GAC ATC 682
Val Arg His Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile
195 200 205
GAC TCG CTG GAA TCC ATC GCC GAC AAG AAC ACC ACC GCG ATG GTC ATC 730
Asp Ser Leu Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala Met Val Ile
210 215 220
ATA AAC CCA AAC AAT CCG TGC GGC AGC GTT TAC TCC TAC GAC CAT CTG 778
Ile Asn Pro Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu
225 230 235
GCC AAG GTC GCG GAG GTG GCA AGG AAG CTC GGA ATA TTG GTG ATC GCT 826
Ala Lys Val Ala Glu Val Ala Arg Lys Leu Gly Ile Leu Val Ile Ala
240 245 250 255
GAC GAG GTT TAC GGC AAA CTG GTT CTG GGC AGC GCG CCG TTT ATC CCG 874
Asp Glu Val Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro
260 265 270
ATG GGC GTC TTT GGG CAC ATT GCC CCG GTC TTG TCC ATT GGA TCT CTG 922
Met Gly Val Phe Gly His Ile Ala Pro Val Leu Ser Ile Gly Ser Leu
275 280 285
TCC AAG TCG TGG ATA GTG CCT GGA TGG CGA CTT GGA TGG GTG GCG GTG 970
Ser Lys Ser Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val
290 295 300
TAC GAC CCC ACA AAG ATT TTA GAG AAA ACT AAG ATC TCT ACG TCT ATT 1018

09025400:021998
866T20:00492060

Tyr Asp Pro Thr Lys Ile Leu Glu Lys Thr Lys Ile Ser Thr Ser Ile
305 310 315
ACG AAT TAC CTT AAT GTC TCA ACG GAC CCA GCA ACC TTC GTT CAG GAA 1066
Thr Asn Tyr Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Val Gln Glu
320 325 330 335
GCT CTT CCT AAA ATT CTT GAG AAC ACA AAA GCA GAT TTC TTT AAG AGG 1114
Ala Leu Pro Lys Ile Leu Glu Asn Thr Lys Ala Asp Phe Phe Lys Arg
340 345 350
ATT ATT GGT CTA CTA AAG GAA TCA TCA GAG ATA TGT TAT AGG GAA ATA 1162
Ile Ile Gly Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Arg Glu Ile
355 360 365
AAG GAA AAC AAA TAT ATT ACG TGT CCA CAC AAG CCA GAA GGA TCG ATG 1210
Lys Glu Asn Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met
370 375 380
TTT GTA ATG GTC AAA CTA AAC TTA CAT CTT TTA GAG GAG ATC CAT GAC 1258
Phe Val Met Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile His Asp
385 390 395
GAC ATA GAT TTT TGC TGC AAG CTC GCA AAG GAA GAA TCA GTA ATT TTA 1306
Asp Ile Asp Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu
400 405 410 415
TGT CCA GGG AGT GTT CTT GGA ATG GAA AAT TGG GTC CGT ATT ACT TTT 1354
Cys Pro Gly Ser Val Leu Gly Met Glu Asn Trp Val Arg Ile Thr Phe
420 425 430
GCC TGC GTT CCA TCT TCT CTT CAA GAT GGA CTC GAA AGG GTC AAA TCA 1402

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Ala Cys Val Pro Ser Ser Leu Gln Asp Gly Leu Glu Arg Val Lys Ser

435

440

445

TTC TGT CAA AGG AAC AAG AAG AAT TCT ATA AAT GGT TGT TAG 1447

Phe Cys Gln Arg Asn Lys Lys Lys Asn Ser Ile Asn Gly Cys

450

455

460 461

TTGTACACAC CCCTAGTTGT ACATCTGACT GAAGCTGTAA ATCATTCTA GTTATCCCCC 1507

ATTATATAT TTCAATAAAA CATATTGTAA TGGTTCTGTT GTAGCTGTCC AAGTCATGTA 1567

CTCTACTTTT TGATGTATTT GGCCTCATTG CCTTGCATCA ATTTCAATAA AAATGGTTGT 1627

GTACACCAAA AAAAAAAAAA AAAAAAAAAA AAA 1660

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1910 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY:

(ii) MOLECULAR TYPE: cDNA to mRNA

(iii) HYPOTHETICAL:

(iv) ANTI-SENSE:

(v) FEATURE: CDS

(vi) LOCATION: 76 .. 1731

(vii) IDENTIFICATION METHOD: P

(viii) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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CGCGCTACTA GTAGTATTCC TGGTGTAGTC TAGTAGTACT CTCCTCCTCC TCCTTCTCCT 60
CCTACCCGTT TCCTC ATG GCC ACC GTA CGC CAG AGC GAC GGA GTC GCC GCG 111
Met Ala Thr Val Arg Gln Ser Asp Gly Val Ala Ala
1 5 10
AAC GGC CTT GCC GTG GCC GCA GCC GCG AAC GGC AAG AGC AAC GGC CAT 159
Asn Gly Leu Ala Val Ala Ala Ala Ala Asn Gly Lys Ser Asn Gly His
15 20 25
GGC GTG GCT GCC GCC GTG AAC GGC AAG AGC AAC GGC CAT GGC GTG GAT 207
Gly Val Ala Ala Ala Val Asn Gly Lys Ser Asn Gly His Gly Val Asp
30 35 40
GCC GAC GCG AAC GGC AAG AGC AAC GGC CAT GGC GTG GCT GCC GAC GCG 255
Ala Asp Ala Asn Gly Lys Ser Asn Gly His Gly Val Ala Ala Asp Ala
45 50 55 60
AAC GGC AAG AGC AAC GGC CAT GCC GAG GCC ACT GCG AAC GGC CAC GGC 303
Asn Gly Lys Ser Asn Gly His Ala Glu Ala Thr Ala Asn Gly His Gly
65 70 75
GAG GCC ACT GCG AAC GGC AAG ACC AAC GGC CAC CGC GAG ACG AAC GGC 351
Glu Ala Thr Ala Asn Gly Lys Thr Asn Gly His Arg Glu Ser Asn Gly
80 85 90
CAT GCT GAG GCC GCC GAC GCG AAC GGC GAG AGC AAC GAG CAT GCC GAG 399
His Ala Glu Ala Ala Asp Ala Asn Gly Glu Ser Asn Glu His Ala Glu
95 100 105
GAC TCC GCG GCG AAC GGC GAG AGC AAC GGC CAT GCG GCG GCG GCG GCA 447
Asp Ser Ala Ala Asn Gly Glu Ser Asn Gly His Ala Ala Ala Ala Ala

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110	115	120	
GAG GAG GAG GAG GCG GTG GAG TGG AAT TTC GCG GGT GCC AAG GAC GGC	495		
Glu Glu Glu Glu Ala Val Glu Trp Asn Phe Ala Gly Ala Lys Asp Gly			
125	130	135	140
GTG CTG GCG GCG ACG GGG GCG AAC ATG AGC ATC CGG GCG ATA CGG TAC	543		
Val Leu Ala Ala Thr Gly Ala Asn Met Ser Ile Arg Ala Ile Arg Tyr			
145	150	155	
AAG ATC AGC GCG AGC GTG CAG GAG AAG GGG CCG CGG CCC GTG CTG CCG	591		
Lys Ile Ser Ala Ser Val Gln Glu Lys Gly Pro Arg Pro Val Leu Pro			
160	165	170	
CTG GCC CAC GGG GAC CCG TCC GTG TTC CCG GCC TTC CGC ACG GCC GTC	639		
Leu Ala His Gly Asp Pro Ser Val Phe Pro Ala Phe Arg Thr Ala Val			
175	180	185	
GAG GCC GAG GAC GCC GTC GCC GCC GCC GTG CGC ACC GGC CAG TTC AAC	687		
Glu Ala Glu Asp Ala Val Ala Ala Ala Val Arg Thr Gly Gln Phe Asn			
190	195	200	
TGC TAC CCC GCC GGC GTC GGC CTC CCC GCC GCA CGA AGC GCC GTG GCA	735		
Cys Tyr Pro Ala Gly Val Gly Leu Pro Ala Ala Arg Ser Ala Val Ala			
205	210	215	220
GAG CAC CTG TCG CAG GGC GTG CCG TAC ATG CTA TCG GCC GAC GAC GTC	783		
Glu His Leu Ser Gln Gly Val Pro Tyr Met Leu Ser Ala Asp Asp Val			
225	230	235	
TTC CTC ACC GCC GGC GGG ACC CAG GCG ATC GAG GTC ATA ATC CCG GTG	831		
Phe Leu Thr Ala Gly Gly Thr Gln Ala Ile Glu Val Ile Ile Pro Val			

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240	245	250	
CTG GCC CAG ACC GCC GGC GCC AAC ATT CTG CTC CCC AGG CCA GGC TAC			879
Leu Ala Gln Thr Ala Gly Ala Asn Ile Leu Leu Pro Arg Pro Gly Tyr			
255	260	265	
CCA AAC TAC GAG GCG CGC GCC GCG TTC AAC AGG CTG GAG GTC CGG CAT			927
Pro Asn Tyr Glu Ala Arg Ala Ala Phe Asn Arg Leu Glu Val Arg His			
270	275	280	
TTC GAC CTC ATC CCC GAC AAG GGG TGG GAG ATC GAC ATC GAC TCG CTG			975
Phe Asp Leu Ile Pro Asp Lys Gly Trp Glu Ile Asp Ile Asp Ser Leu			
285	290	295	300
GAA TCC ATC GCC GAC AAG AAC ACC ACC GCC ATG GTC ATC ATA AAC CCC			1023
Glu Ser Ile Ala Asp Lys Asn Thr Thr Ala MeT Val Ile Ile Asn Pro			
305	310	315	
AAC AAC CCG TGC GGC AGC GTT TAC TCC TAC GAC CAT CTG TCC AAG GTC			1071
Asn Asn Pro Cys Gly Ser Val Tyr Ser Tyr Asp His Leu Ser Lys Val			
320	325	330	
GCG GAG GTG GCG AAA AGG CTC GGA ATA TTG GTG ATT GCT GAC GAG GTA			1119
Ala Glu Val Ala Lys Arg Leu Gly Ile Leu Val Ile Ala Asp Glu Val			
335	340	345	
TAC GGC AAG CTG GTT CTG GGC AGC GCC CCG TTC ATC CCA ATG GGA GTG			1167
Tyr Gly Lys Leu Val Leu Gly Ser Ala Pro Phe Ile Pro Met Gly Val			
350	355	360	
TTT GGG CAC ATC ACC CCT GTG CTG TCC ATA GGG TCT CTG TCC AAG TCA			1215
Phe Gly His Ile Thr Pro Val Leu Ser Ile Gly Ser Leu Ser Lys Ser			

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365	370	375	380	
TGG ATA GTG CCT GGA TGG CGG CTT GGA TGG GTA GCG GTG TAC GAC CCC	1263			
Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Val Ala Val Tyr Asp Pro				
385	390	395		
AGA AAG ATC TTA CAG GAA ACT AAG ATC TCT ACA TCA ATT ACG AAT TAC	1311			
Arg Lys Ile Leu Gln Glu Thr Lys Ile Ser Thr Ser Ile Thr Asn Tyr				
400	405	410		
CTC AAT GTC TCG ACA GAC CCA GCA ACC TTC ATT CAG GCA GCT CTT CCT	1359			
Leu Asn Val Ser Thr Asp Pro Ala Thr Phe Ile Gln Ala Ala Leu Pro	415			
420	425			
CAG ATT CTT GAG AAC ACA AAG GAA GAT TTC TTT AAG GCG ATT ATT GGT	1407			
Gln Ile Leu Glu Asn Thr Lys Glu Asp Phe Phe Lys Ala Ile Ile Gly				
430	435	440		
CTG CTA AAG GAA TCA TCA GAG ATA TGC TAG AAA CAA ATA AAG GAA AAC	1455			
Leu Leu Lys Glu Ser Ser Glu Ile Cys Tyr Lys Gln Ile Lys Glu Asn				
445	450	455	460	
AAA TAC ATT ACA TGT CCT CAC AAG CCA GAA GGA TCA ATG TTT GTC ATG	1503			
Lys Tyr Ile Thr Cys Pro His Lys Pro Glu Gly Ser Met Phe Val Met				
465	470	475		
GTG AAA CTG AAC TTA CAT CTT TTG GAG GAA ATA GAC GAT GAC ATT GAT	1551			
Val Lys Leu Asn Leu His Leu Leu Glu Glu Ile Asp Asp Asp Ile Asp				
480	485	490		
TTT TGC TGC AAG CTC GCA AAA GAA GAA TCA GTA ATC TTA TGC CCA GGG	1599			
Phe Cys Cys Lys Leu Ala Lys Glu Glu Ser Val Ile Leu Cys Pro Gly	495			

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500 505
AGT GTT CTT GGA ATG GCA AAC TGG GTC CGC ATT ACT TTT GCT TGT GTT 1647
Ser Val Leu Gly Met Ala Asn Trp Val Arg Ile Thr Phe Ala Cys Val
510 515 520
CCA TCT TCT CTT CAA GAT GGT CTC GGA AGG ATC AAA TCA TTC TGT CAA 1695
Pro Ser Ser Leu Gln Asp Gly Leu Gly Arg Ile Lys Ser Phe Cys Gln
525 530 535 540
AGG AAC AAG AAG AGA AAT TCG AGC GAT GAT TGC TAG TTGTATATCT 1741
Arg Asn Lys Lys Arg Asn Ser Ser Asp Asp Cys
545 550 551
GACTGAAGCT GTAAATCATT CCCAGTATCC CCATCTATAT CTTTCAATAA AATGGAACCT 1801
TTAGTTCTCT ATGAATAGAA GTCAACATCT CCTTGAATAT GTTCTGGTTG TTGTGGCCTG 1861
GACGAAACAT AGTGAATGTT ATGTTAGTGA AGTTAAAAA AAAAAAAAAA 1910

(6) INFORMATION FOR SEQ ID NO: 5:

Primer 1: 5'-GCIGTIGARTGGAAYTTYGCIMG-3'

Primer 2: 5'-GCDATRTGICCRAAIACICC-3'

wherein R, Y, M and D are mixed bases shown below and I is inosine,

R=A/G, Y=C/T, M=A/C and D=A/T/G.